

DRAFT NUMBER: 100-100

Signal peptide

A5.

homology
region

1	atggatgtggcgccgctgcgttgcctgttttagctctctggcttcgtacccgtgg	60
1	[M D V A A A A L P A F V A L W L L Y P W]	20
61	cctctcctggggctggcccttggCcagttctcagcagggtggctgtactttgtatggg	120
21	P L L G S] A L G Q F S A [G G C T F D D G	40
121	ccaggggcttgtgactaccaccaggattatacgatgacttgagtgggtccatgtcagt	180
41	P G A C D Y H Q D L Y D D F E W V H V S	60
181	ggcaggaaacctcattacctgcggggCgaaatgcctcaagggttccatatgggtgtGac	240
61	A Q E P H Y L P P E M P Q G S Y M V V D	80
241	tcctcaaattcatgatcctggagaaaaagccagacttcagtcgtgcctaccatgaaggagaat	300
81	S S N H D P G E K A R L Q L P T M K E N	100
301	gacaccactgcattgattcagttacccgttatatacgccagaagggttgcaccctggc	360
101	D T H C I D F S Y L L Y S Q K G L N P G	120
361	acttgaatatccttagttgggtgaaataaggaccttgcataatccaatttggaatgta	420
121	T L N I L V R V N K G P L A N P I W N V	140
421	actggattcactggcgtgattggctccggctgaactagtcgtgagcacccccc	480
141	T G F T G R D W L R A E L A V S T F W P	160
481	aatgaataccaggtaatatttgaagctgaagtcgtcaggaggagaagtggatattgcc	540
161	N E Y Q V I F E A E V S G G R S G Y I A	180
541	attgatgacatccaagtccgttgcataatctccatccgccttgcgttatccgcctt	600
181	I D D I Q V L S Y P C D K S P H F L R L	200
601	ggtgatgtggagggtcaatgtggcagaatGCTacatttcagtcattgcataaggaga	660
201	G D V E V N A G Q N A T F Q C I A T G R	220
661	gatGCTgTGcataacaaggatggctgcagagacgcataatggtagcc	720
221	D A V H N K L W L Q R R N G E D I P V A	240
721	cagactaagaacataaatcacaagatgtgcgttgcatttcagattgcataaggaga	780
241	Q T K N I N H R R F A A S F R L Q E V T	260
781	aaaactgaccaggatttgaccgtgcgtactcagtcagaacgagggtctgggttcc	840
261	K T D Q D L Y R C V T Q S E R G S G V S	280

FIG. 1(1)

DRAFT VERSION 1.000001

841	aattttgtcaactcattgtgagagaaccacccatggctcccccagctgctt	900
281	N F A Q L I V R E P P R P I A P P Q L L	300
901	ggtgttgggcctacttaacttgcgtatccaactaaatgccaactctattattggcgatggc	960
301	G V G P T Y L L I Q L N A N S I I G D G	320
961	ccccatcatcctgaaagaagttagatcgaaatgacatcaggatcttggacagaaaacccat	1020
321	P I I L K E V E Y R M T S G S W T E T H	340
1021	gcagtcaacgcaccaacataaagtgtggcatttagaccagatacagaatacggatc	1080
341	A V N A P T Y K L W H L D P D T E Y E I	360
1081	cgcgtcctgcttaccagacacctggcgaaaggggactggctgccaggaccaccactgatc	1140
361	R V L L T R P G E G G T G L P G P P L I	380
1141	actagaacgaagtgtcgagaacctatgcggacaccaaagactttaaagattgctgaaatc	1200
381	T R T K C A E P M R T P K T L K I A E I	400
1201	caggcaaggcgcatgtcagtggactggagtccttggctacaacatcactcggtgccac	1260
401	Q A R R I A V D W E S L G Y N I T R C H	420
1261	actttcaacgtcaactatctgttaccattacttccgtggccacaatgagagcaggcagac	1320
421	T F N V T I C Y H Y F R G H N E S R A D	440
1321	tgcttgacatggacccaaagccccctcagcatgttgcataaccatctgccacccatcaca	1380
441	C L D M D P K A P Q H V V N H L P P Y T	460
1381	aatgtcagcctcaagatgatcctaaccacccagagggaaaggagagcgaagagaca	1440
461	N V S L K M I L T N P E G R K E S E E T	480
1441	atcatccaaactgtatgaaagatgtccccggcctgtgccagtcaaatccctccaagaaca	1500
481	I I Q T D E D V P G P V P V K S L Q G T	500
1501	tcctttgaaaacaagatcttcctgaaactggaaagagccactggaaaccgaaatggattatc	1560
501	S F E N K I F L N W K E P L E P N G I I	520
1561	actcagtatgaggtgagctatacgacataagatcatggaccctgtgtccaggct	1620
521	T Q Y E V S Y S S I R S F D P A V P V A	540
1621	gggcccccacagactgtatcaaatttatgaaatagtacacaccatgtatcatctt	1680
541	G P P Q T V S N L W N S T H H V F M H L	560
1681	caccctggaaaccacccatccaggaaaaataagagccagCactgtcaaaggcttggacca	1740
561	H P G T T Y Q F F I R A S T V K G F G P	580

FIG. 1(2)

0 0 0 0 0 0 0 0 0 0

Trans-
membrane

1741	gcaacagccatcaatgtgaccacaaaatctcagctccaagcttacactgactatgaagga	1800
581	A T A I N V T T N I S A P S L P D Y E G	600
1801	gttgatgcctctctgaatgaaactgccaccaccatcacagtactattggggcctgcacaa	1860
601	V D A S L N E T A T T I T V L L R P A Q	620
1861	gccaaagggtgtcttatcagtgttatcaaattttgtggagcagctacacccacatcgaa	1920
621	A K G A P I S A Y Q I V V E Q L H P H R	640
1921	acgaaggcgtgaaggcaggggccatggaatgttaccaggtaaccggttacataccagaacgc	1980
641	T K R E A G A M E C Y Q V P V T Y Q N A	660
1981	ctaagtggggGcgcgCcattactttgtccgcagaacttccccctggaatcttcccgg	2040
661	L S G G A P Y Y F A A E L P P G N L P E	680
2041	cctgtcccttcaccgtgggtgacaacccgacataaaggctttggaaaccttcccgt	2100
681	P A P F T V G D N R T Y K G F W N P P L	700
2101	gccccccgcaaaggataacaacatctatccaaaggcatgagcgtgtggagaaggaaact	2160
701	A P R K G Y N I Y F Q A M S S V E K E T	720
2161	aaaacccaaatgtgtacgaattgttacaaaaggcagcagcaacAgaagaaccagaagtgt	2220
721	K T Q C V R I A T K A A A T E E P E V I	740
2221	ccagacccggcaaaGCagacagacagactggtaaaaatcgccggCatcagtgtggcatc	2280
741	P D P A K Q T D R V V K [I A G I S A G I	760
2281	ctagtgttcatcccttcctgtgtgtcatagtaattgtggaaaaagagaaggcaagcttgc	2340
761	L V F I L L L V V I V K K S K L A]	780
2341	aagaaggcacaagatgcaatgggaacacacgtcaggagatgacccacatggtaatgt	2400
781	K K R K D A M G N T R Q E M T H M V N A	800
2401	atggaccgaagttatgttaccagagcaccctgtcatgcagaagaccccttccctacc	2460
801	M D R S Y A D Q S T L H A E D P L S L T	820
2461	ttcaTggaccaacataacttcagtcacatggccatgttgcactggccactgg	2520
821	F M D Q H N F S P R L P N D P L V P T A	840
2521	gtgttagatgagaaccacagtgccacacgcatgttgcgtctCctggatgttccctoga	2580
841	V L D E N H S A T A E S S R L L D V P R	860

FIG. 1(3)

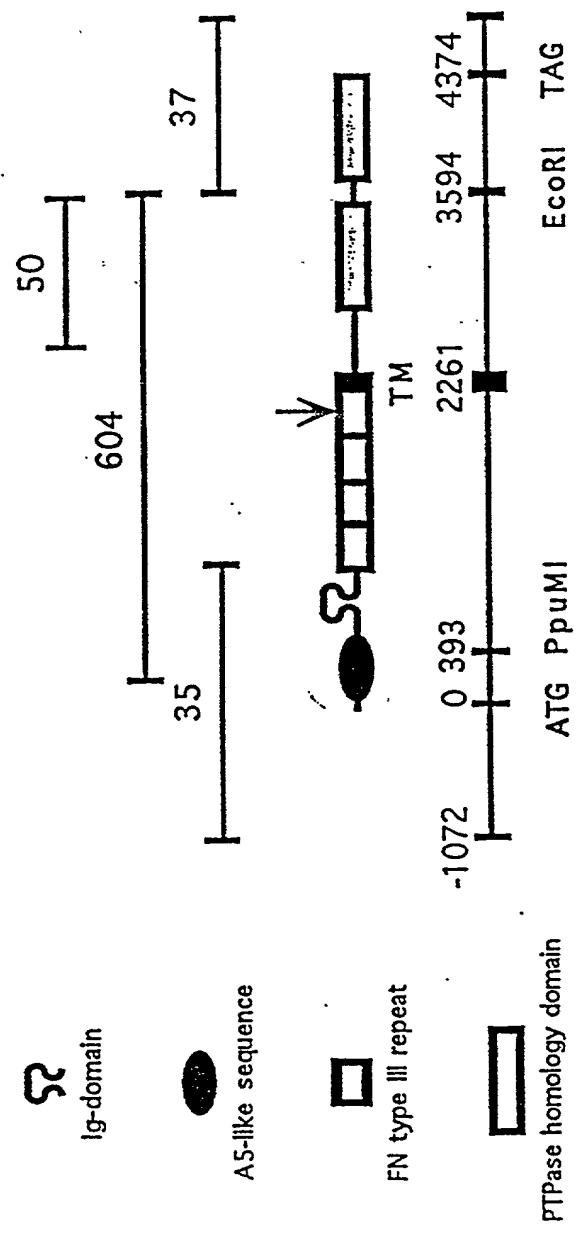
2581	tacctctgcgaaggcacagactcccttatcagacaggacagctgcacccagccatcagg	2640
861	Y L C E G T E S P Y Q T G Q L H P A I R	880
2641	gtggccgacttaactgcagcacattaacctcatgaagacatcagacagactatgggttcaa	2700
881	V A D L L Q H I N L M K T S D S Y G F K	900
2701	gaggaatacggagCttctttgaaggccagtgcgccttggatgtggctaaaaaggat	2760
901	E E Y E S F F E G Q S A S W D V A K K D	920
<i>PTPase Domain I</i>		
2761	caaaacagagcaagaaccgatacgaaacattatcgcatatgatcactccagagtcatc	2820
921	Q N R A K [N R Y G N I I A Y D H S R V I	940
2821	ctgcaacctgtgaaagatgacccttcttcagattacattaatgccaactacatcgacatt	2880
941	L Q P V E D D P S S D Y I N A N Y I D I	960
2881	tggctgtacaggatggctaccagagaccaagccactacattGCaactcaaggcccagt	2940
961	W L Y R D G Y Q R P S H Y I A T Q G P V	980
2941	catgaaaccgtatatgatttttGGAggatggtgtggcaagagcagtcgtgcctgtatttg	3000
981	H E T V Y D F W R M V W Q E Q S A C I V	1000
3001	atggtcactaaTtagtgGaagtTGGCCGggtaaatgctataatattggcctgtatgat	3060
1001	M V T N L V E V G R V K C Y K Y W P D D	1020
3061	actgaggttatggacttcaaagtcaCTGCgtaaaatggagccacttgctgagttat	3120
1021	T E V Y G D F K V T C V E M E P L A E Y	1040
3121	gtcgtaggacattcaccttggaaaggaggggctataatgaaatccgtgaagtcaaacag	3180
1041	V V R T F T L E R R G Y N E I R E V K Q	1060
3181	ttccacttcactggctggcctgaccatgggtttccataccacgcacaggcctctgtca	3240
1061	F H F T G W P D H G V P Y H A T G L L S	1080
3241	tttatccggagagtcaagctatctaaccctcccagtgcgtggccattgtcgtaactgc	3300
1081	F I R R V K L S N P P S A G P I V V H C	1100
3301	agtgcgtggctggcgcacaggctgttacattgttattgacataatgctggacatggct	3360
1101	S A G A G R T G C Y I V I D I M L D M A	1120
3361	gaaagagagggtgtggtgcacatctacaactgtgtgaaagccttacgatctcggcgcatt	3420
1121	E R E G V V D I Y N C V K A L R S R R I	1140
3421	aatatggtacagacagaggaacagtcattttattcatgatgccatggctgc	3480
1141	N M V Q T E E Q Y I F I H D A I L E] A C	1160

FIG. 1(4)

3481	ttatgtggagaaactgccatccctgtgtgaatttaaagctgcataaaaaatgatt	3540
1161	L C G E T A I P V C E F K A A Y F D M I	1180
3541	cgaatagacttcagactaactcctcatctcaaaagatgaatttcagactctgaattcg	3600
1181	R I D S Q T N S S H L K D E F Q T L N S	1200
3601	gtcacccctcgactacaagactgaagactgcagcatagccgcctgccaaggaccatgac	3660
1201	V T P R L Q A E D C S I A C L P R [N] H D	1220
3661	aagaaccgtttcatggatatgtcccacctgacagatgtctgcctttttaaattacaatt	3720
1221	K N R F M D M L P P D R C L P F L I T I	1240
3721	gatggggagagCagtaactacatcaatgctgctttatggatagctataggcagccagca	3780
1241	D G E S S N Y I N A A L M D S Y R Q P A	1260
3781	gctttcatgtCacacaatacccaactgccaaacactgtgaaagacttCtggagatttagta	3840
1261	A F I V T Q Y P L P N T V K D F .W R L V	1280
3841	tatgattAaggatgtacccatcgatgctaaatgaagtggacctgtctcaggcgtgc	3900
1281	Y D Y G C T S I V M L N E V D L S Q G C	1300
3901	ccacagtactggccagaagaaggaaatgctgcgatatggccttatccaagtggaaatgtatg	3960
1301	P Q Y W P E E G M L R Y G P I Q V E C M	1320
3961	tcttgttcaatggactgtgatgtgatcaatcgaaatggatcgaaacctaacgaga	4020
1321	S C S M D C D V I N R I F R I C N L T R	1340
4021	ccacaggaggctatctgatggtacaacagTTCCagtacctaggctggcttcatcg	4080
1341	P Q E G Y L M V Q Q F Q Y L G W A S H R	1360
4081	gaagtgcctggctccaaacgcgtcgaaaaatgatactgCagggtggaaaaatggcaa	4140
1361	E V P G S K R S F L K L I L Q V E K W Q	1380
4141	gaggaatgtgaagaaggggaaaggccggacaatcatccactgcttgaatggcggtggCC	4200
1381	E E C E E G E G R T I I H .C L N G G G R	1400
4201	agtggcatgttctgtccataggcattgttgaggatggtaagcggaaaaatgtgggt	4260
1401	S G M F C A I G I V V E M V K R Q N V V	1420
4261	gatgtttccatgcagtaaaagacgcgtggaaacagcaagccaaacatggtggaaagccccg	4320
1421	D V F H A V K T L R N S K P N M V E A P	1440
4321	gagcaatgtatcgTtttgcataatgtatgtggcgtagacttgcgtgcctcatag	4374
1441	E Q Y R F C Y D V A L E Y L E S S * S S	1458

FIG. 1(5)

FIG. 2



卷之三

3
FIG.

* * * * * PQL L GVGPTYLILQLNANS I IGDGPILLKEVE Y RMTSGSWTETHAVNAAPTYKLWHLDPDTE.YEIRVLL T R PG EG C TGLPGPPLITRT
II (392) P .KT L KIAEIQA..RRIAVD W ESLGYNITRCHT F NYTICYHYFRGHNESRADCLMDPKA...PQHVVNH L P PY TN V SLMKIL.TNPEG
III (493) P VKS L QCTSFE...NKIFLN W KEPLEPNGLITQ Y EWSYSSISTRSEDPAVPVAGPPQTVSNLWNNSTHHVFMH L H PG TT Y QFFIRASTVKGF
IV (596) P DYE G VDASLNETATITVL L RPAQAKGAPISA Y QIVVEQLHPRTKR.EAGAMECYQV....PVTYQNA L S GG AP Y YFAAEELPPGNLP
FBN-III(7) P PTN L HIeanPDT.GVLTUS W ERSTTPD. ITG Y RITTTPTINGCCGNSLEEVVHADQ.....SSCTFDN L S PG LE Y NVSVY..TVKDD

FIG. 4

PTP- κ (34)
PTP- μ (26)
A5 (651)
Consensus

GGCTFDGPGACDYHQLDYDDEFWVVAQE. PHYLPPPEMPQGSYMWVQDSSNHDPCGKARLQLPTMKEN. DTHCIDEFSVLLYSQK
GGCLFDEPYSTCGYSQADEDDFNWEQVNTLTKPT. SDPWMPSGSFMLVNNTSGKPE. QRAHLLIPQLKEN. DTHCIDEFYFVSSKS
CKFGWCSQKTVCNWQHDISSDLKWAVLN SKTGP. VQDHHTGDNFIYSEADERHECRAARLMSPVVSSRSAAHCLTFWYHM. . . D
C---D---W---N---T---P---G---F---E---ARL---P---H---F---Y---

PTP- κ
PTP- μ
A5
Consensus

GLNPCTLNLVRVN. KGPLANPIIWNVTGFTGRDWLRALAVSTFWPNEXQVIFEA. VSGGRSGYIAIDDIQVLSY
NAAPGLNLNVVKVN. NGPLGNPIIWNISGDPTRTWRALATSTFWPNFYYQVIFEV. VTSQGHQGYLAIDEVKVLGH
GSHVGTLSIKLKYEMEEDFDQTLMTVSGNQGDQWMEARVVLHKTMKQ. YQVIVEC. VCGKGSAGGIAVDDIIIANH
G---GTL-I---K---W-VSG---G---W-A---YQVI-E---V---G---G-IA-DDI---H

FIG. 5

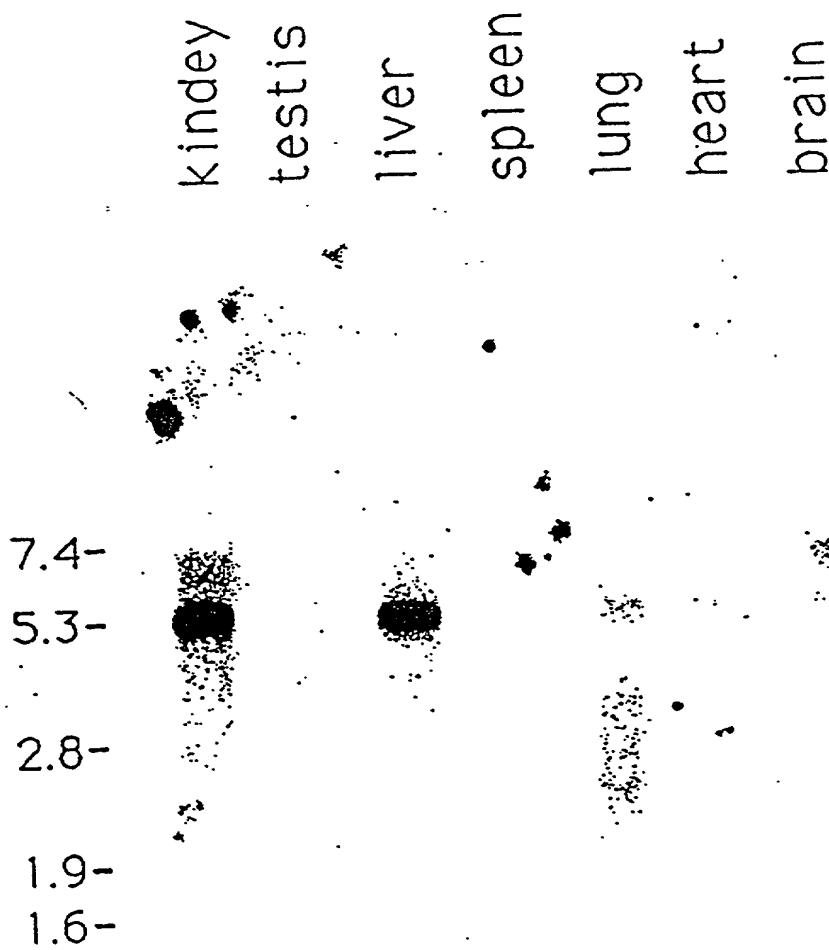


FIG. 6

Transfected: - - - + + +
Antibody: pre α - κ α - κ pre α - κ α - κ
Peptide: - - + - - +

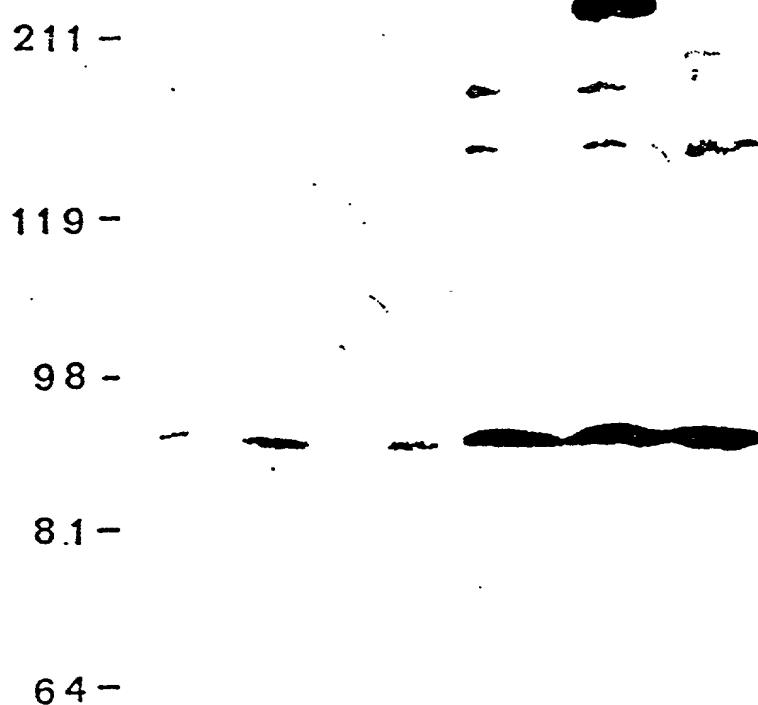
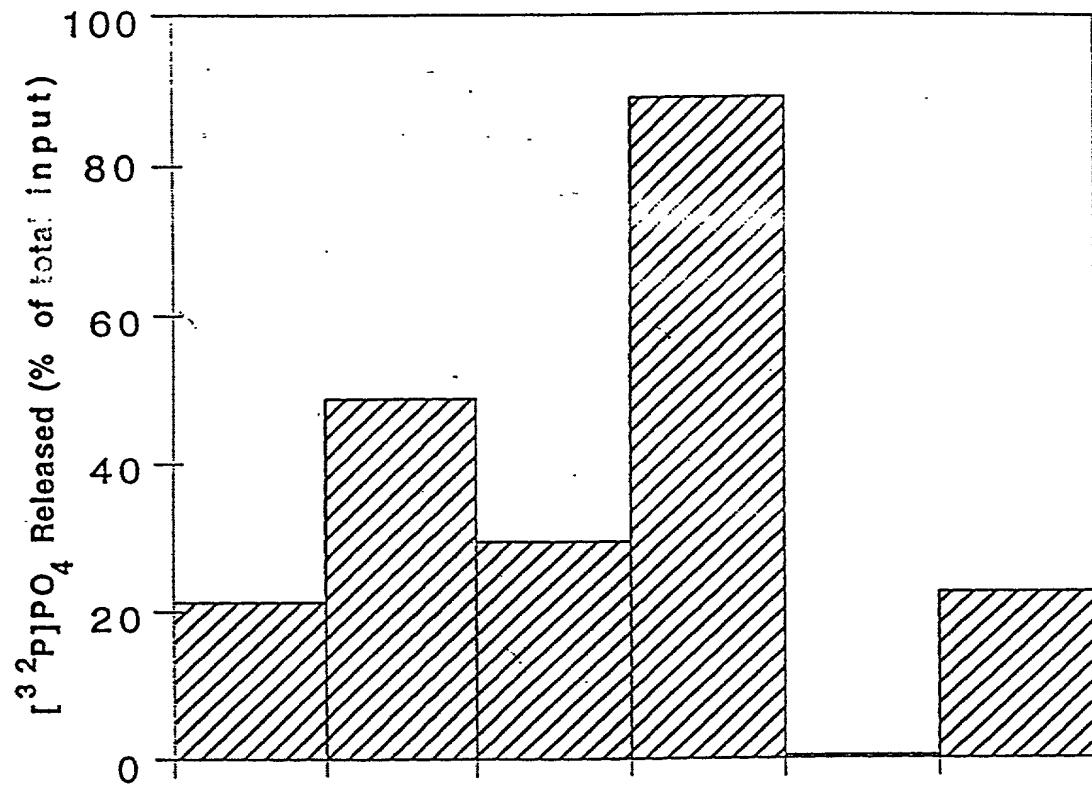


FIG. 7



Transfection	mock	κ	mock	κ	mock	κ
Antibody	pre	pre	116	116	116	116
Vanadate	-	-	-	-	+	+

FIG. 8

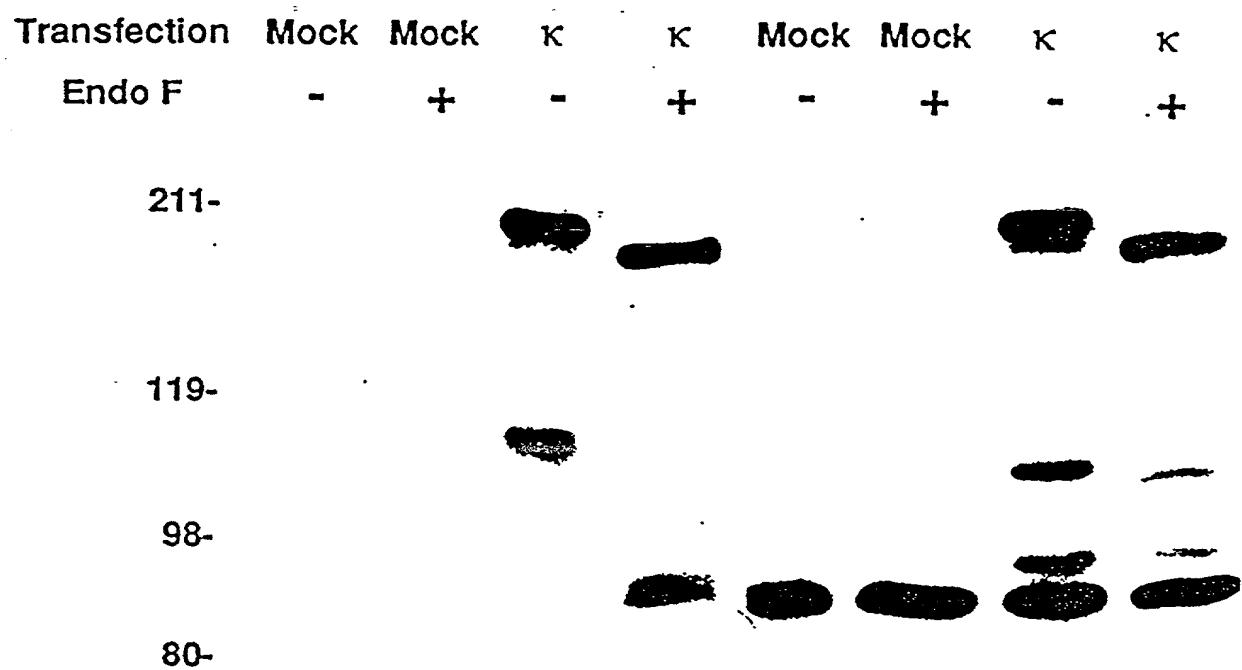


FIG. 9

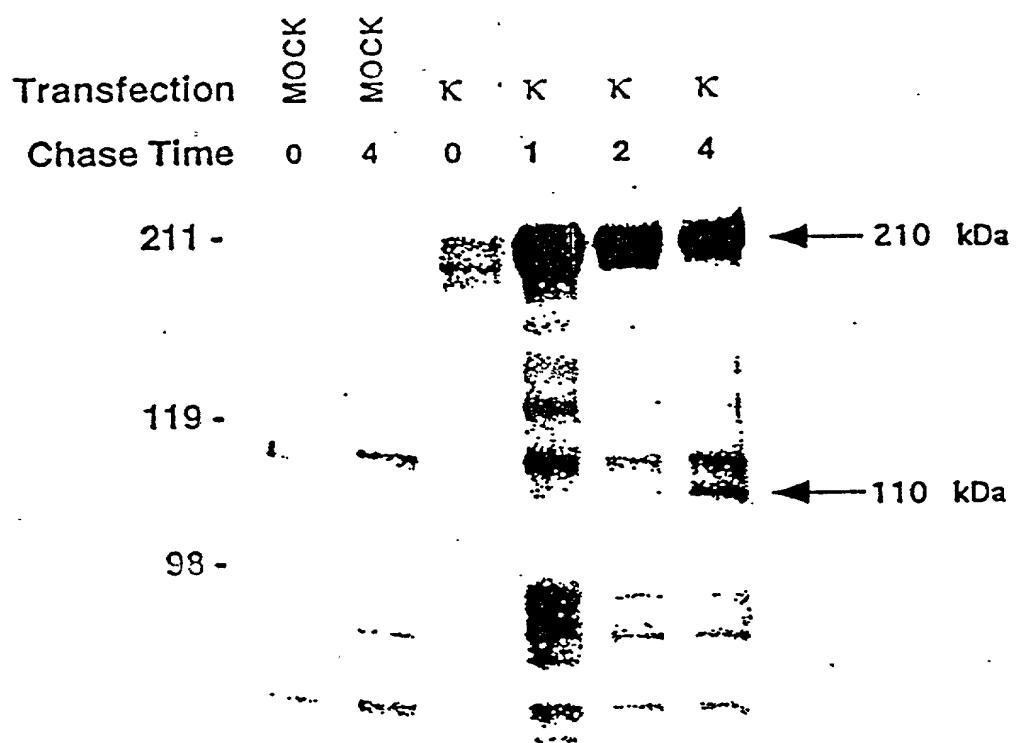


FIG. 10

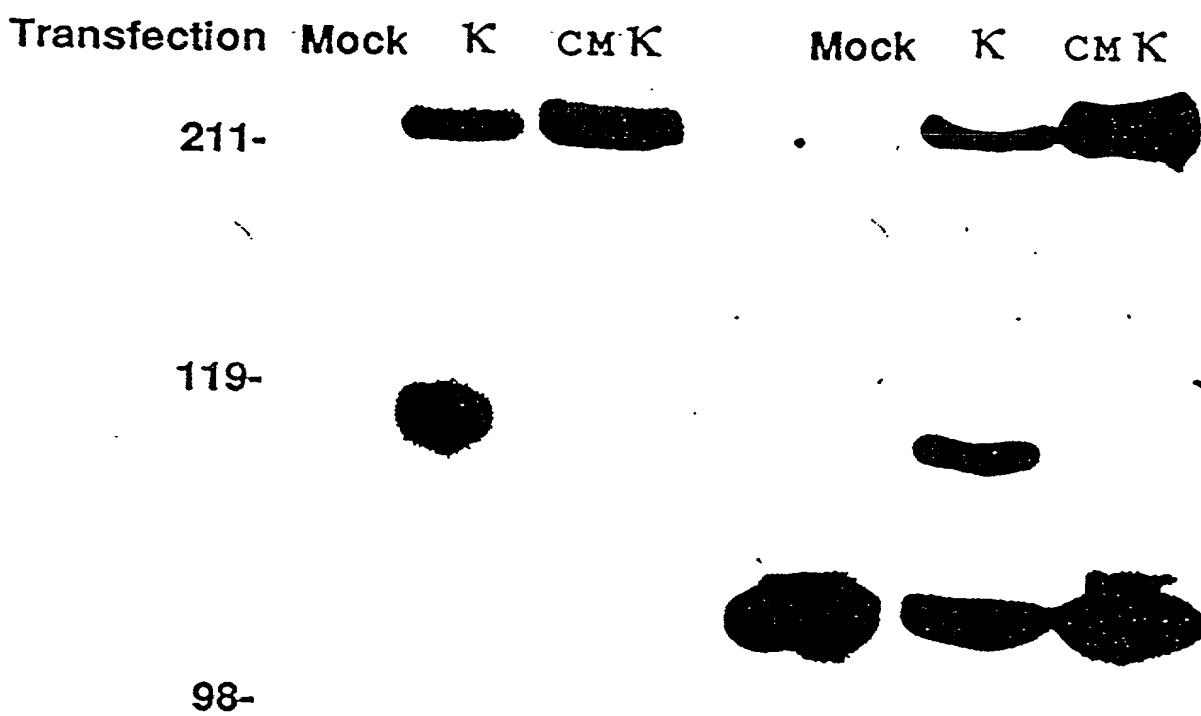


FIG. 11

Transfection Mock K K
IP 116 116 Total
lysate

211-



119-



98-



FIG. 12

000000000000000000000000

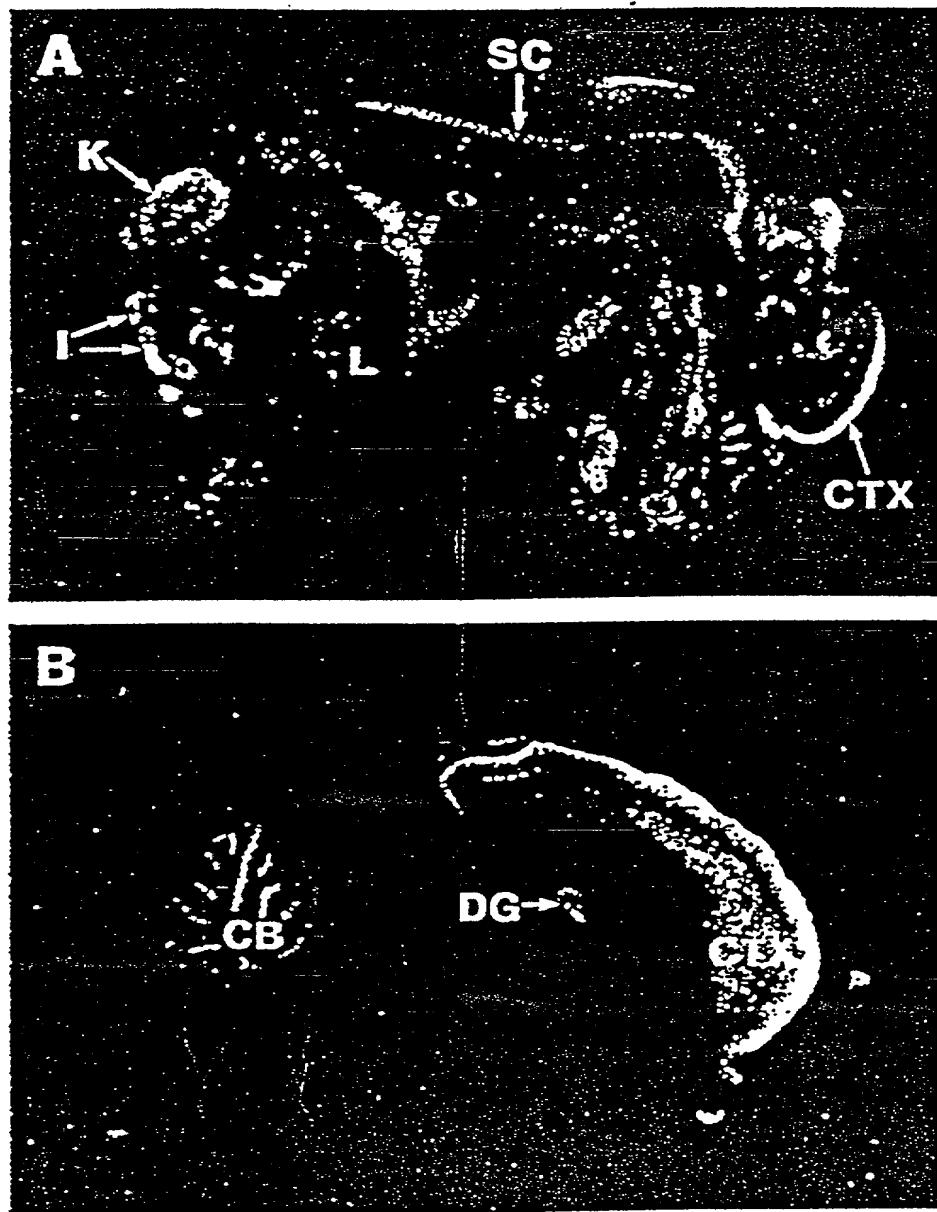


FIG. 13

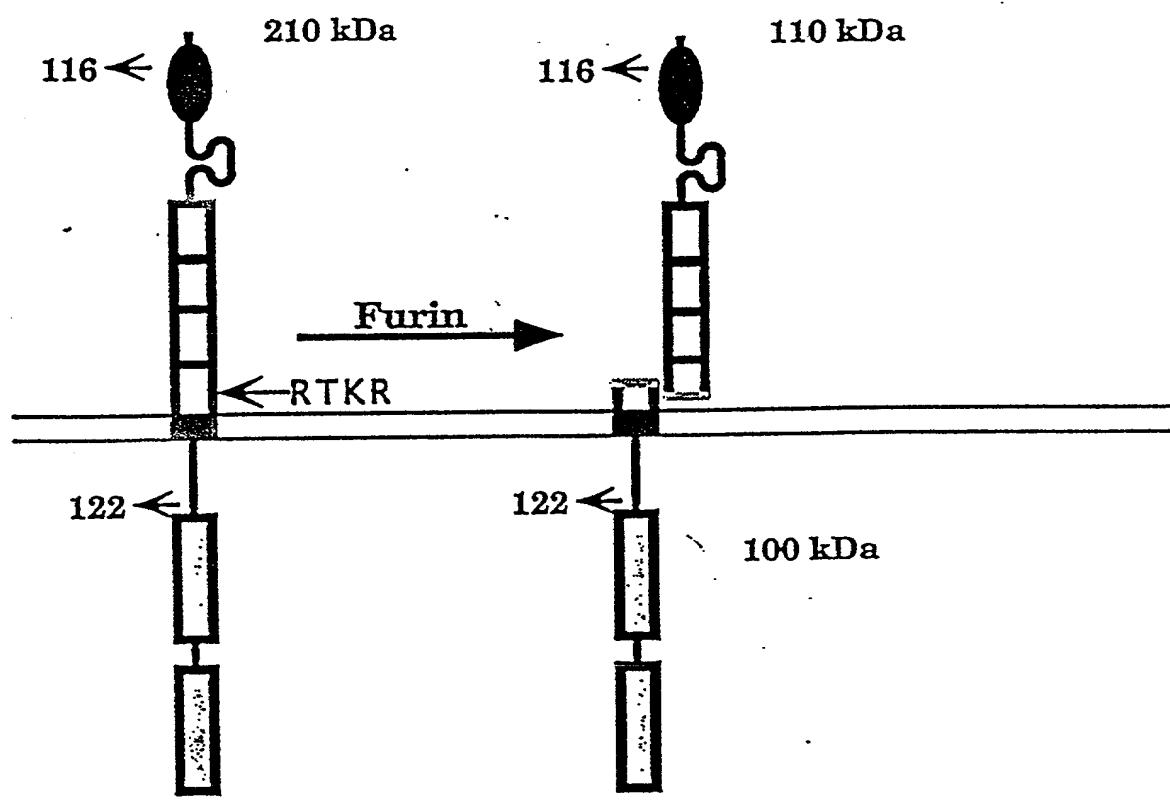


FIG. 14

1 ATGGATACTGGCGCCGGCGCTGCCCTGCTTTGTGGCCCTTGCTCCCTCTCCTGGCTCTCTGGATGGC 80
 -1 M D T T A A A A L P A F V A L L L S P W P L L G S A 27
 81 CCAAGGCCAGTCTCCGCAGGTGGCTGACTTTGATGATGGCCAGGGCCGTGATTACCAACCAGGATCTGTATGATG 160
 27 Q G Q F S A G G C T F D D G P G A C D Y H Q D L Y D D 53
 161 ACTTTGAATGGGTGCATGTTAGTGGCTCAAGAGCCCTCATTATCTACCAACCCGAGATGCCCAAGGTTCCATATGATAGT 240
 54 F E W V H V S A Q E P H Y L P P E M P Q G S Y M I V 80
 241 GACTCTTCAGATCACGACCCCTGGAGAAAAGCCAGACTTCAGTGCCTACAACTGAAAGGAGAACACTCACTGCATTGA 320
 81 D S S D H D P G E K A R L Q L P T M K E N D T H C I D 107
 321 TTTCAGTTACCTTATATAGCCAGAAAGGACTGAATCCCTGGCACTTTGAACATATTAGTTAGGGTGAATAAAGGACCTC 400
 107 F S Y L L Y S Q K G L N P G T L N I L V R V N K G P L 133
 401 TTGCCAATCCAATTGGAATGTGACTGGATTACGGTAGAGATTGGCTCCGGCTGAGCTAGCAGTGACCCCTTTGG 480
 134 A N P I W N V T G F T G R D W L R A E L A V S T F W 160
 481 CCCAATGAATTCAGGTAATATTGAGCTGAAGTCTCAGGAGGGAGAAGTGGTTATATTGCCATTGATGACATCCAAGT 560
 161 P N E Y Q V I F K A E V S G G R S G Y I A I D D I Q V 187
 561 ACTGAGTTATCCTTGATAAATCTCCTCATTTCTCCGTCTAGGGATGTAAGGGTAATGCAGGGCAAACGCTACAT 640
 187 L S Y P C D K S P H F L R L G D V E V N A G Q N A T F 213
 641 TTCAGTGCATTGCCACAGGGAGAGATGCTGCTACAAAGTTATGGCTCCAGAGACGAAATGGAGAAGATAACAGTA 720
 214 Q C I A T G R D A V H N X L W L Q R R N G E D I P V 240
 721 GCCCCAGACTAAGAACATCAATCATAGAAGGTTGCCCTCCCTCAGATTGCAAGAAGTGCACAAAAACTGACCAGGATT 800
 241 A Q T K N I N H R R F A A S F R L Q E V T K T D Q D L 267
 801 GTATCGCTGTGTAACTCAGTCAGAACGAGGTTCCGGTGTGCTCAATTGGCTCAACTTATGTGAGAGAACGCCAAGAC 880
 267 Y R C V T Q S E R G S G V S N F A Q L I V R E P P R P 293
 881 CCATTGGCTCCTCCCTCAGCTTCTGGTGTGGCCTACATATTGCTGATCCAACATAATGCCAARCTCGATCATGGCGAT 960
 294 I A P P Q L L G V G P T Y L L I Q L N A N S I I G D 320
 961 GGTCTTATCATCTGAAAGAAGTAGAGTACCGAATGACATCAGGATCCTGGACAGAAACCATGCACTGCAATGCTCCAAC 1040
 321 G P I I L K E V E Y R M T S G S W T E T H A V N A P T 347
 1041 TTACAAATTATGCCATTAGATCCAGAACATGGAAATGAGATCCAGTTCTACACTAACAGCTGGTGAAGGTGGAACGG 1120
 347 Y K L W H L D P D T E Y E I R V L L T R P G E G G T G 373
 1121 GGCTCCAGGACCTCCACTAATCACCAAGAACAAATGTGCAAGAACCTATGAGAACCCAAAGACATTAAGATTGCTGAA 1200
 374 L P G P P L I T R T K C A E P M R T P K T L K I A E 400
 1201 ATACAGGCAAGACGGATTGCTGTGGACTGGAAATcCTTGGTTACAACATTACCGTTGCCACACTTTAAATGTCAT 1280
 401 I Q A R R I A V D W E S L G Y N I T R C H T F N V T I 427
 1281 CTGCTACCATTACTTCCGTGGTACAACCGAGAGCAAGGAGACTGTTGGACATGGACCCCAAAGCCCTCAGCATGTTG 1360
 427 C Y H Y F R G H N E S K A D C L D M D P K A P Q H V V 453
 1361 TGAACCATCTGCCACCTTATACAAATGTCAAGATGATCCTAACCAATCAGAGGGAGGAAGGAGAGTGAAGAG 1440
 454 N H L P P Y T N V S L K M I L T N P E G R K E S E E 480
 1441 ACAATTATTCAAACTGATGAAGATGTGCCCTGGCCCTACCAAGTAAATCTCTCAAGGAACATCCTTGAAATAAGAT 1520
 481 T I I Q T D E D V P G P V P V K S L Q G T S F E N K I 507
 1521 CCTCTTGAACTGGAAAGAACCTTGGATCAAATGGAATCATCACTCAATATGAGATCAGCTATGAGCTATAAGATCAT 1600
 507 F L N W K E P L D P N G I I T Q Y E I S Y S S I R S F 533
 1601 TTGATCTGCAGTCCCAGTGGCTGGACCTCCCCAGACTGTATCAAATTATGGAACAGTACACACCATGCTTTATGCAT 1680
 534 D P A V P V A G P P Q T V S N L W N S T H H V F M H 560
 1681 CTCCACCCCTGGAACCGTACCAAGCTTCTGATCAAAGGCCAGCACGGTCAAGGCTTGGTCCAGGCCAGCCATCAATGT 1760
 561 L H P G T T Y Q F F I R A S T V K G F G P A T A I N V 587
 1761 CACCAACATATCTCAGCTCAACTTACCTGACTATGAAGGAGTTGATGCCCTCTCAATGAAACTGCCACCACAAATAA 1840
 587 T T N I S A P T L P D Y E G V D A S L N E T A T T I T 613
 1841 CTGTATTGTTGAGACCAGCACAAGCCAAAGGTGCTCTATCAGTGCTTATCAGATTGTTGGAAGAAGTGCACCCAC 1920
 614 V L L R P A Q A K G A P I S A Y Q I V V E E L H P H 640

1921	CGAACCAAGAGAGAACGCCGAGCCATGGAATGCTACCAAGGTTCCCTGTACATACCAAARTGCCATGAGTGGGGTGCACC	2000
641	R T K R E A G A M E C Y Q V P V T Y Q N A M S G G A P	667
2001	GTATTACTTGGCTGAGAACTACCCCCGGAAACCTACCTGAGCCTGCCCGTTCAGTGGGTGACAATCGGACCTACC	2080
667	Y Y F A A E L P P G N L P E P A P F T V G D N R T Y Q	693
2081	AAGGCTTTGGAACCTCCTTGGCTCCCGCAAAGGATAACACATCTATTCCAGGGCATGAGCAGTGTGGAGAAGGAA	2160
694	G F W N P P L A P R K G Y N I Y F Q A M S S S V E K E	720
2161	ACTAAAACCCAGTGCCTACGCATTGCTACAAAAGCAGAACAGAAGAAGCAGACTGATCCCAGATCCCGCAAGCAGAC	2240
721	T K T Q C V R I A T K A A T E E P E V I P D P A K Q T	747
2241	AGACAGAGTGGTAAAAATAGCAGGAATTAGTGCCTGGAAATTGGTGTTCATCCTCCTCTCTAGTTGTCATATTAATTG	2320
747	D R V V K I A G I S A G I L V F I L L L L V V I L I V	773
2321	AAAAAAAGAGCARACTTGCTAAAAAACGAAAGATGCCATGGGAATACCCGGCAGGAGATGACTCACATGGTGAATGCA	2400
774	K K S K L A K K R K D A M G N T R Q E M T H M V N A	800
2401	ATGGATCGAAGTTATGCTGATCAGAGCACTCTGCATGCAGAAAGATCCTCTTCATCACCTTCATGGACCAACATAACTT	2480
801	M D R S Y A D Q S T L H A E D P L S I T F M D Q H N F	827
2481	TAGTCCAAGATATGAGAACCACAGTGCCTACAGCAGAGTCCAGTCGCCTCTAGACGTACCTCGCTACCTCTGTGAGGGGA	2560
827	S P R Y E N H S A T A E S S R L L D V P R Y L C E G T	853
2561	CGGAATCCCTTACCAAGACAGCAGCTGCATCCAGGCATCAGGGTAGCTGATTTACTGCAGCACATTAACTCATGAG	2640
854	E S P Y Q T G Q L H P A I R V A D L L Q H I N L M K	880
2641	ACATCAGACAGCTATGGGTTCAAAGAGGAATATGAGAGCTTTTGAGGACAGTCAGCATCTGGGATGTAGCTAAAAA	2720
881	T S D S Y G F K E E Y E S F F E G Q S A S W D V A K K	907
2721	AGATCAAAATAGCAAAAACCGATATGAAACATTATAGCATATGATCACTCCAGAGTGATTTGCAACCCGTAGAGG	2800
907	D Q N R A K N R Y G N I I A Y D H S R V I L Q P V E D	933
2801	ATGATCCTCCTCAGATTATATTAAATGCCACTATATTGATGGCTACCAAGAGACCAAGTCATTACATTGCAACCCAAAGGT	2880
934	D P S S D Y I N A N Y I D G Y Q R P S H Y I A T Q G	960
2881	CCCGTTCATGAAACAGTGTATTTCTGGAGGATGATTTGCAAGAACATCTGCTTGCTATTGATGGTTACAAATT	2960
961	P V H E T V Y D F W R M I W Q E Q S A C I V M V T N L	987
2961	AGTTGAGGTTGGCCGGTTAACCTCTATAATTGGCTGATGATACTGAGTTATGGTACATTCAAAGTACGTGTG	3040
987	V E V G R V K C Y K Y W P D D T E V Y G D F K V T C V	1013
3041	TAGAAATGGAACCACTTGCTGAATATGAGTTAGGACATTCCAGGCTGGAAAGGAGGGGTACAATGAAATCCGTGAAGTT	3120
1014	E M E P L A E Y V V R T F T L E R R G Y N E I R E V	1040
3121	AAACAGTTCCATTACGGGCTGGCCTGACCATGGAGTGCCCTACCATGCTACAGGGCTGCTTCCATTACCGGAGT	3200
1041	K Q F H F T G W P D H G V P Y H A T G L L S F I R R V	1067
3201	CAAGTTATCAAACCCCTCCAGTGCCTGGCCCATCGTTGTACATTGCAGTGCTGGCTGGACGAACGGCTGCTACATTG	3280
1067	K L S N P P S A G P I V V V H C S A G A G R T G C Y I V	1093
3281	TGATTGACATCATGCTAGACATGGCTGAAAGAGAGGGTGTGTTGATATTACAATTGTCAGGCTTAAGATCTGG	3360
1094	I D I M L D M A E R E G V V D I Y N C V K A L R S R	1120
3361	CCTATTAAATGGTCCAGACAGAGGAACAGTACATTTCATGATGCATTAGAAGGCTGCTATGTGGAGAAC	3440
1121	R I N M V Q T E E Q Y I F I H D A I L E A C L C G E T	1147
3441	TGCCATACCTGTGTGAAATTAAAGCTGCATATTGATGATTAGAATAGACTCCCAGACTAACCTCACATCTCA	3520
1147	A I P V C E F K A A A Y F D M I R I D S Q T N S S H L K	1173
3521	AGGATGAATTTCAGACTCTGAATTCACTGACTACAGCTGAAGACTGCAGTATAGCGTGCCTGCCAGAAC	3600
1174	D E F Q T L N S V T P R L Q A E D C S I A C L P R N	1200
3601	CATGACAAGAACGGTTCATGGACATGCTGCCACCTGACAGATGTCGCTTCTTAAATTACAATTGATGGGAGAGCAG	3680
1201	H D K N R F M D M L P P D R C L P F L I T I D G E S S	1227
3681	TAACTACATCAATGCTGCTTATGGACAGCTACAGGCAACCGCTGCTTCACTGTCACACAATACCCCTGCCAAACA	3760
1227	N Y I N A A L M D S Y R Q P A A F I V T Q Y P L P N T	1253
3761	CTGTAAAAGACTTCTGGAGATTAGTGTATGATTGGCTGACCTCCATTGATGTTAAACGAAGTGCAGTGTCCAG	3840
1254	V K D F W R L V Y D Y G C T S I V M L N E V D L S Q	1280

3841 GGCTGCCCTCAGTACTGGCCAGAGGAAGGGATGCTACGATATGGCCCCATCCAAGTGGAAATGTATGTCTGTTCAATGGA 3920
 1281 G C P Q Y W P E E G M L R Y G P I Q V E C M S C S M D 1307

3921 CTGTGATGTGATCAACCGGATTTTAGGATATGCAATCTAACAAAGCACACAGGAAGGTTATCTGATGGTCAACAGTTTC 4000
 1307 C D V I N R I F R I C N L T R P Q E G Y L M V Q Q F Q 1333

4001 AGTACCTAGGATGGCCTCTCATCGAGAAGTGCCTGGATCCAAAGGTCAATTCTGAAACTGATACTTCAGGTGGAAAAG 4080
 1334 Y L G W A S H R E V P G S K R S F L K L I L Q V E K 1360

4081 TGGCAGGAGGAATGCCAGGAAGGGAGGCCGGAGCATTATCCACTGCCTAAATGGTGGCGGGCGAAGTGGCATGTTCTG 4160
 1361 W Q E E C E E G E G R T I I H C L N G G G R S G M F C 1387

4161 TGCTATAGGCATCGTTGAAATGGTGAACGGCAAAATGTTGCGATGTTCCATGCAGTAAAGACACTGAGGAACA 4240
 1387 A I G I V V E M V K R Q N V V D V F H A V K T L R N S 1413

4241 GCAAGCAAACATGGTGAAGCCCCGGAGCAATACCGTTCTGCTATGATGAGCTTGAGTACCTGGAATCATCTAG 4320
 1414 K P N M V E A P E Q Y R F C Y D V A L E Y L E S S * 1439

4321 TTGGGTGAGACTCTTAAAGTCATCCATGAAGAACCTGTCATCTATTGAGCCAGCAGCTGTTGACCTGTTAACCTT 4400
 4401 GTGCAGAAAGATTTAATGTCGGGGGGGGAGACTTTACATTGAGAGGTAAGATTTTTATGAGTTGTTATGAGTTGTTAT 4480

4481 CTTAATAAAAAGAACTGAATTAGTTTATTACATATTAAGCATCAACATTCATGCCACATAAAATTATATTAAATA 4560

4561 AGAACCGATTGAAATGAGAACGTATTGGTGTGTTGACAGTGAACATGCCACCTTTCCATGGTTCAAGGTAGTCAGC 4640
 4641 TACCACATGTT 4651

(SEQ IO NO: 4)

(SEQ IO
NO: 2)

FIG. 15 (3)

MCP7 hrPTP μ	MDTTAAAALPAPVALLLSPWPPLGSACQGFSAGGCTPDDGPGACDYHQDLYDDPEWVHVSQAEPHYLPPMPQGSYIV -MR LGTC - TL G -----TAAGET - L E PYST G S SEG N EQ NTLT KPTSD W S LL	80 71
MCP7 hrPTP μ	DSSDHDPGEKARLOPLTMKENDTHC1DFSYLLYSQKGLNPGTLN1LVRVNKGPLANPIWNVTGFTGRDWLRALAVSTFW NA GRPE QR H L QL H F VS KSNP L V Y K N G IS DPT T N I	160 151
MCP7 hrPTP μ	PNEYQVIEAEVSGGRSGYIAADDIQLVSLSTPCDRSPHFLRLGDEVNAQONATPQCLATGRDAVNLKLWLRNNGEDIFV F V-ITS HQ L EVK GH TRT IGN F S I TVAGDR GIDVR A L	240 230
MCP7 hrPTP μ	AGTKNINHRRFAASPRLCVTKTDQDLYRCVTQSERGSVSNFAQLIVREPPRPIAPPQILGVGPTYLIIQIANSIIGD KEI VTISS I NVVAT R AGK MIRT G V I Y EVK V AS A W N	320 310
MCP7 hrPTP μ	GPIIILKEVEYRMTSGSWIETHAVNAPTYKHNHLDPTEYEIRVLLTRPGEGGTGCLGPGEPLITRTKCAEPMRIPKTLKIAE VAR CTA NDQP DSTS IG S S AR D GRK EVV	400 390
MCP7 hrPTP μ	IQARRIADVWESLGYNITRCHTFNVTICHYPRGHNE--SKADCLMDPKAPQHVNVHLPPYTNSLKHILINPEGRKES VKS Q TIR FT V SY L VH C QV QQ QVREEVSW TENS H TITN S VL M	478 470
MCP7 hrPTP μ	EETIIQTDEDVPGPVVKSLQGTSFENKIPLNKEPLDPNGLIITQYELISYSSIRSFDPAVPVAGPFPQTVSNIWNSTHRVF Q L V L A TE I ST E Q R TQTY V L T KAVS EIDLSNQSGR K G E PL	558 550
MCP7 hrPTP μ	MHILHPGTTYOFFIRASTVKGPGPATAINVTTNISAPTLPEDYEGVDASINETATTITVLLRPACAKGAPISAYQIVVEELH PG Y S T A PATNQF K SM A -LETP Q DN V M K HSR V V ER	638 629
MCP7 hrPTP μ	PHRTKREAGAMECYQPVUTYQNAMEGGAPYTFAAELP-GNLPEPAPFTVGDNRTYQGFNPFLAPFKGTYIYIQAMSSVE R KTEILK P IIP SLLNSQ F ADS QAAQ I K N Y T LYSR A RAN	718 709
MCP7 hrPTP μ	KETKTCCVRIATKAATEEEPEVDPAKQTIRVVKLAGISAGILVFILLLVILIVKSKLAKKRKDAMGNTQEMTHMV G ID QV G A-T KPV E E BT VI L VIIF G V VM R ET SS V	798 788
MCP7 hrPTP μ	NAMDTSYADQSTILHAEDPSITFMDQHNFSPRY-----ENHSATAESSRLLDWPRY-LCE S K E G -NCDEAF -- T LNG SVSSPSPMTKNTLSTSVPSYYPD T TMASDT S VQSHT KKR	852 865
MCP7 hrPTP μ	GTESPYQTGQLHPAIRVADLLQHINLMKTSYDGFKEEYESPFEGQSASWDVAKKDQNRAKNRGYNIIAYDHSRVILOPV PADV TQ CAEG P S E M R TI	932 945
MCP7 hrPTP μ	EDDPSSOYINANYIDGYCRPSHYIATQGPVHETVYDEWRMIWQEQSACIVMVTNLVEVGRVKCYKWPDDTEVYGDFFKVT G TN G H N MQ I V H NT S I C I K I	1012 1025
MCP7 hrPTP μ	CVEMEPLAEEYVVRTPTLERRGYNEIREVKOFEPHTGPWDHGVPYHATGILSFIRRVKLSNEPSAGPIVVCAGAGRTGCV LI T L I AV K VH IR G V O SKS L F	1092 1105
MCP7 hrPTP μ	IVIDIMLDMAEREGVVDIYNCVKALRSRRINMVQTEEQYTFIHDAILEACLCGETAIPVCEPKAAYFDMIRIDSQTNSSH RE V V D SV ASQVSL Y NKL F Q	1172 1185
MCP7 hrPTP μ	LKDEFQTLNSVTPRLQAEDCSACLPRNHDKNRFMIDLPPDRCLPPLITIDGESSNYINAALMDSYRQPAAPTIVTOYPLP I E R M T RV L E C I K S H	1252 1265
MCP7 hrPTP μ	NTVKDEWRLVYDYGCTSIVMLNEVDLSQLGCPQYWPEEGMLRYGPIQVECMSCSMDCDVINRIFRICNLTRPQEGYLMVQQ L H V D : PA L N VH H PV ADLEE I S Y AA D R	1332 1345
MCP7 hrPTP μ	FQYLGWASHREVPGSKRSZLKLILQVEKWWEECEEGEGRTIIHCLNGGGRSGMPCAIGIVVEMVKPQNVVVDVFAVKTLR F PMY DT V R D YNG P VV T S C LRH RT	1412 1425
MCP7 hrPTP μ	NSKPNMVEAPEQYRFCYDVALEYLESS* N DLLD R E N G *	1439 1452

FIG. 16

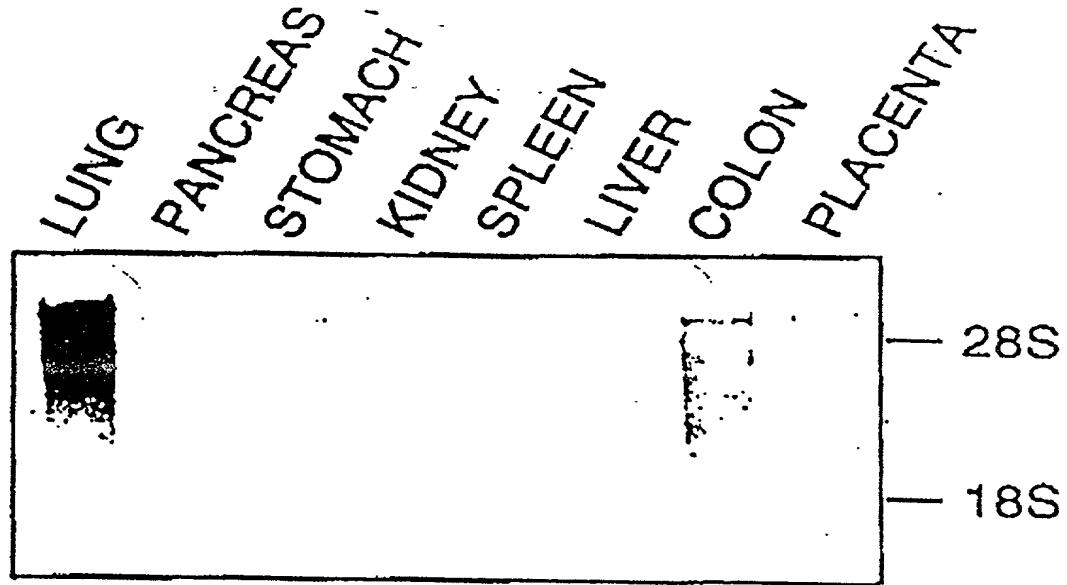


FIG. 17

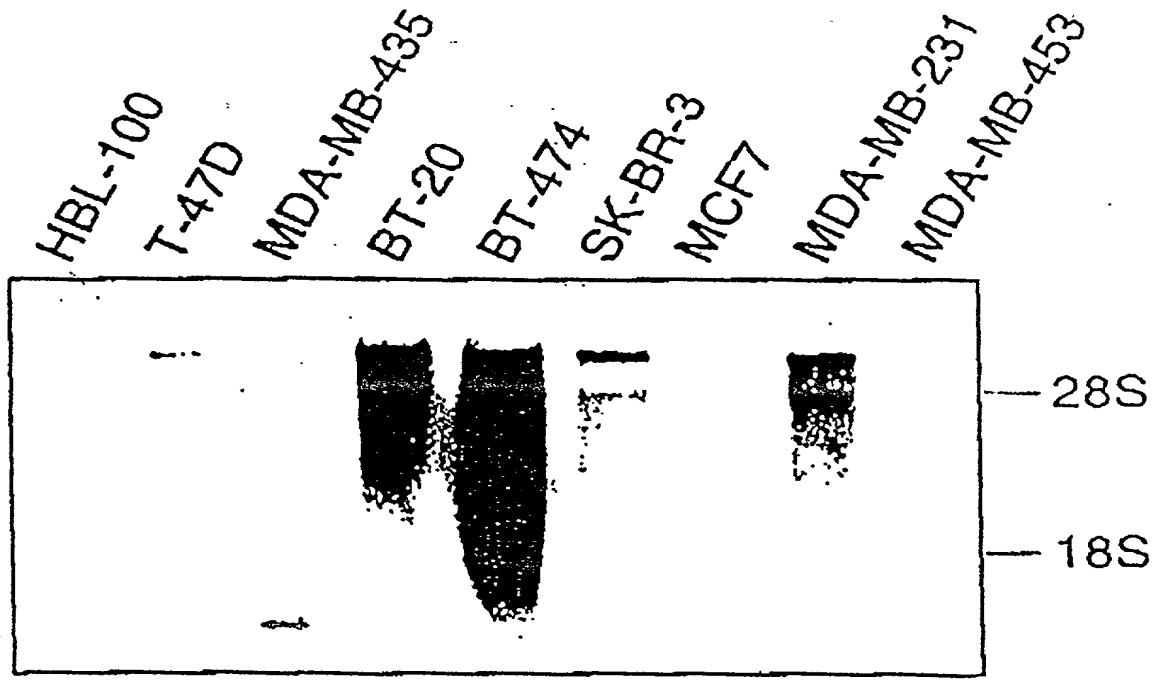


FIG. 18

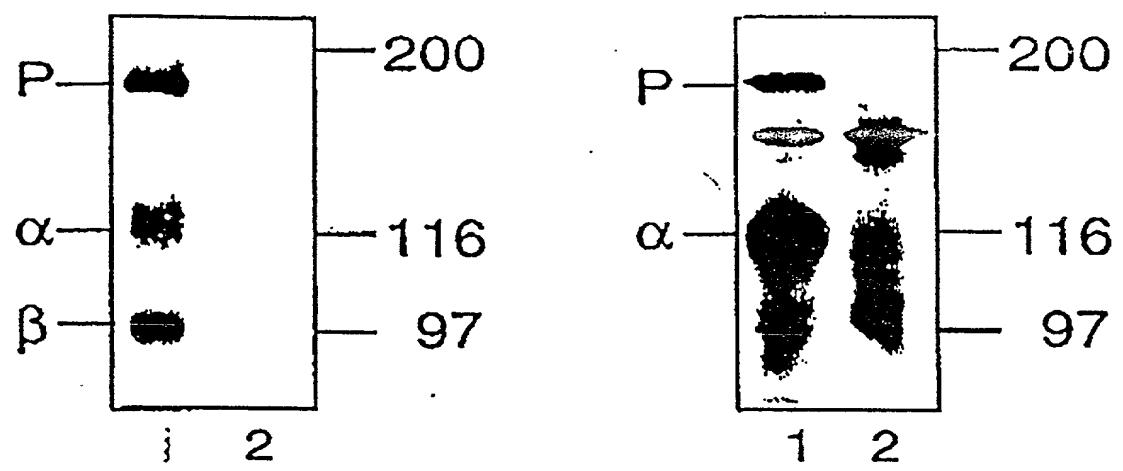


FIG. 19

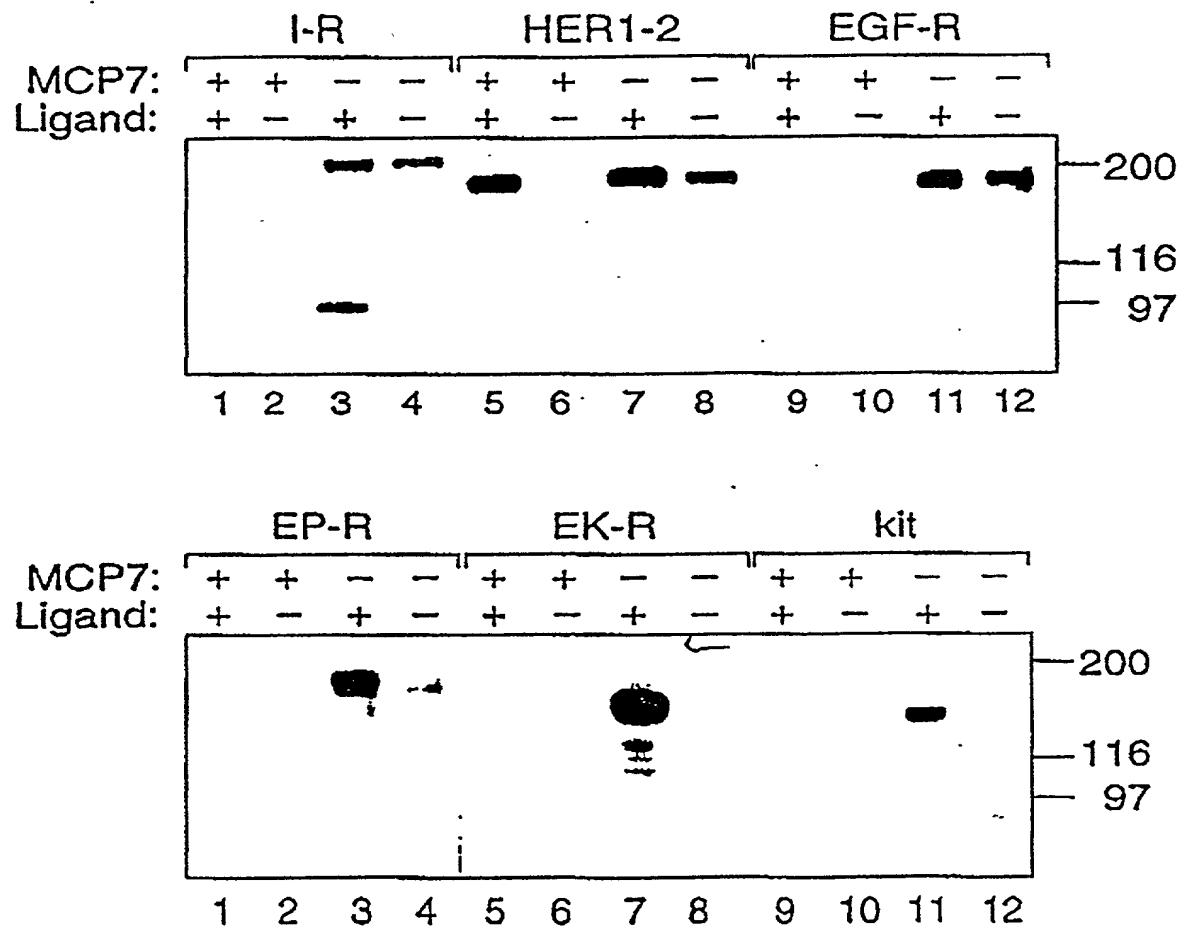


FIG. 20

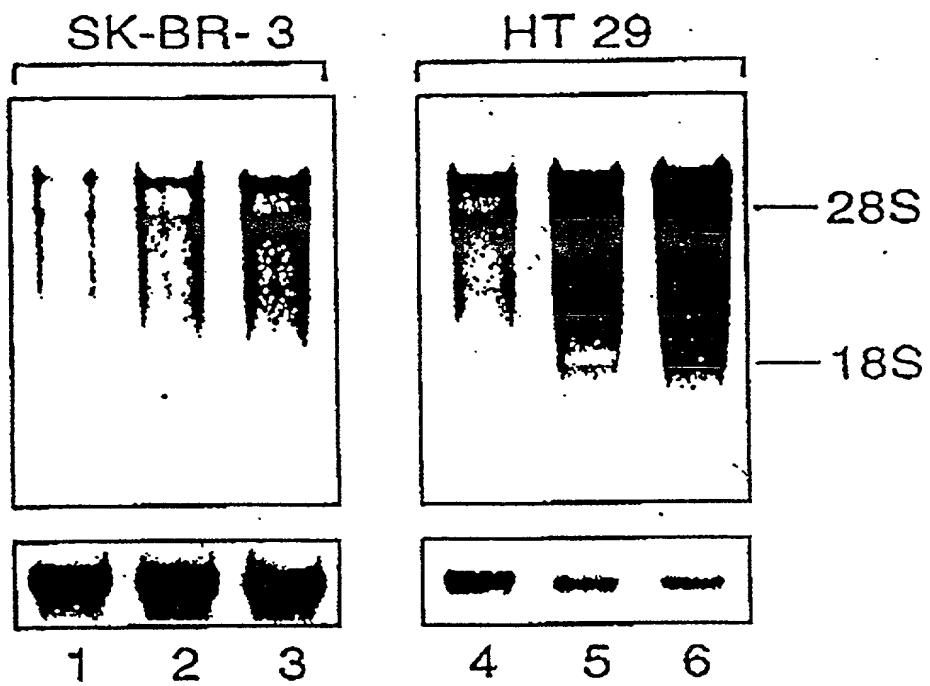


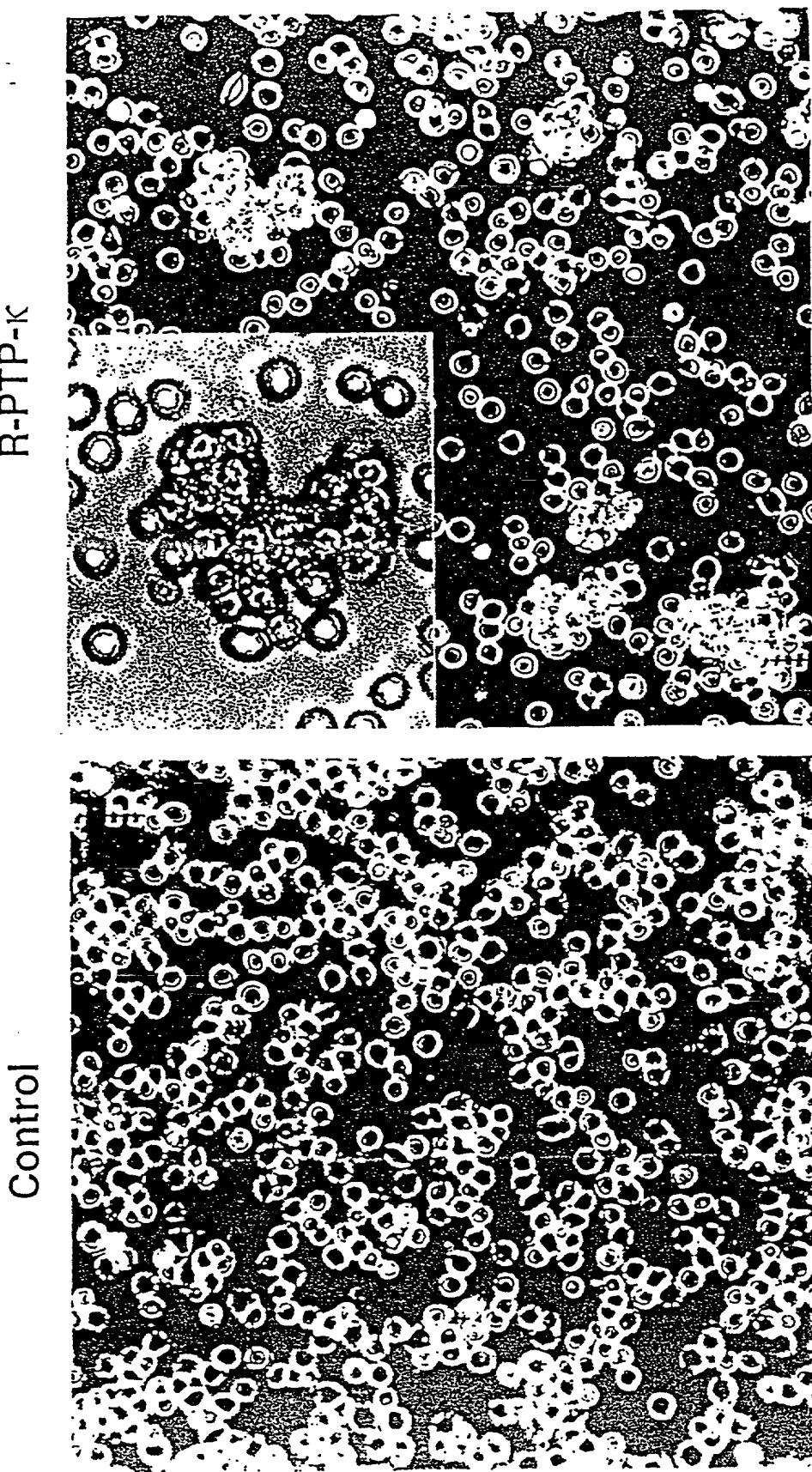
FIG. 21

1 2 3 4 5

190 --
125 --
88 --
65 --
56 --

FIG. 22 A

FIG. 22B



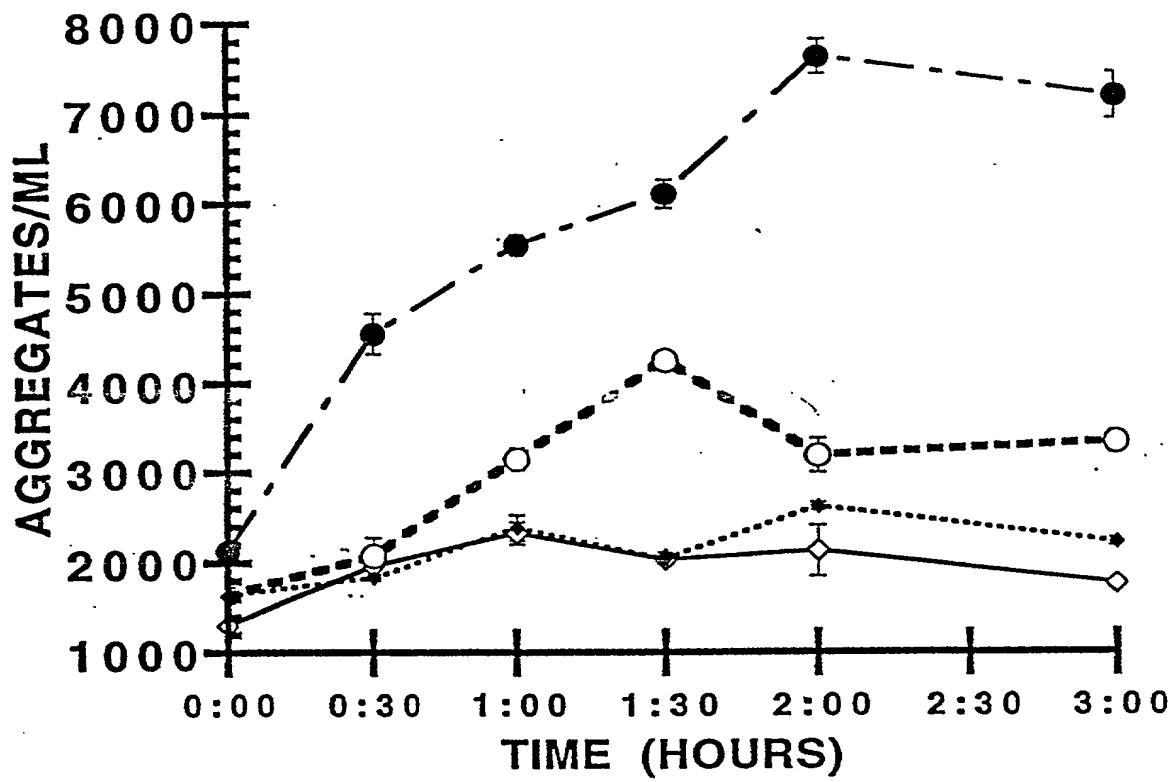


FIG. 22 C

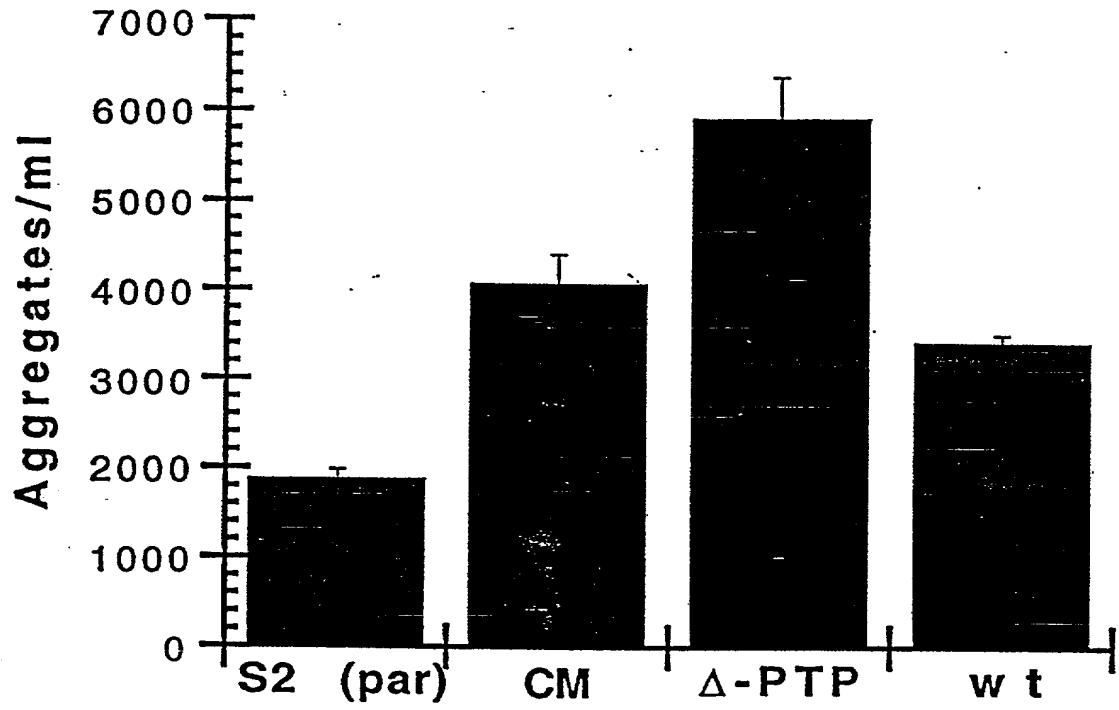
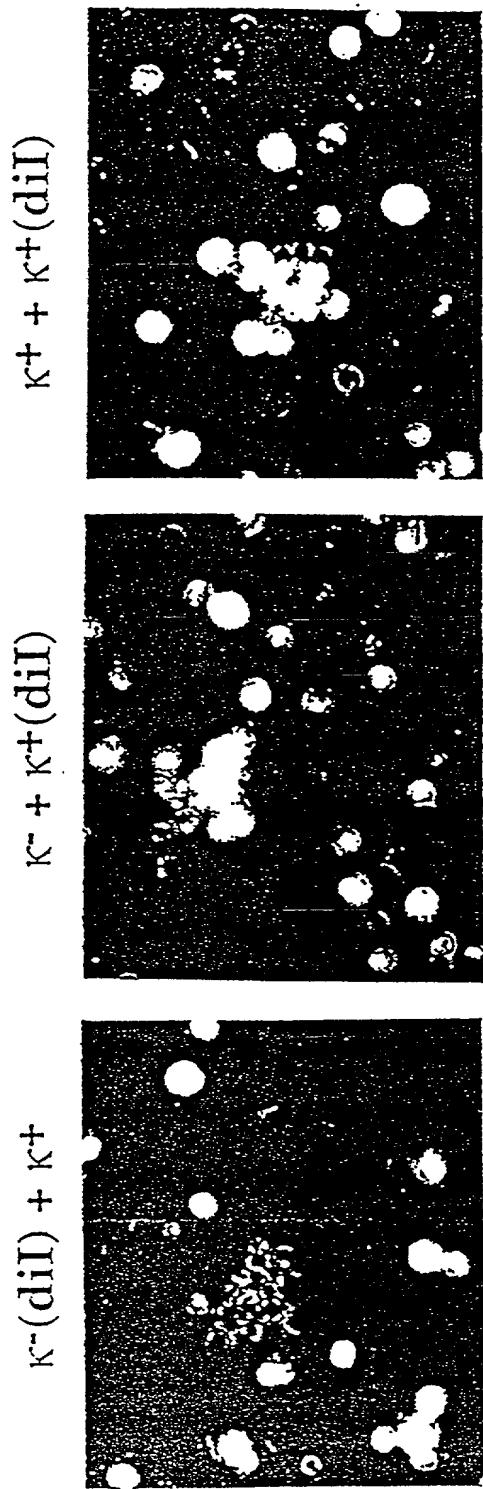


FIG. 22D

FIG. 23



TYPE OF Tissue

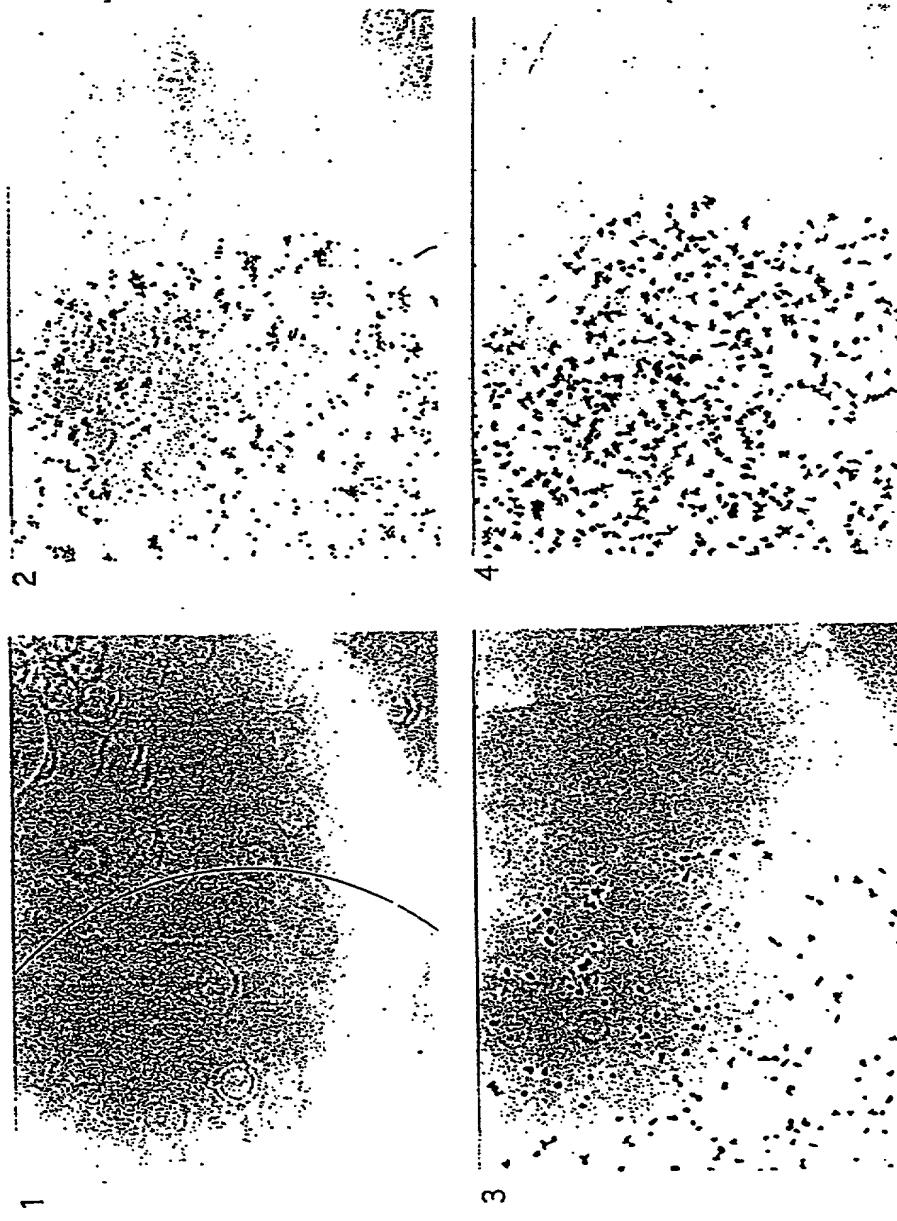


FIG. 24